Welcome to the Synthetic Biology Open Language (SBOL) Developers Workshop

Newcastle University
Newcastle Upon Tyne
August 2016
Programme

- 09:00-09:30 Overview of SBOL – Anil Wipat
- 09:30-10:00 SBOL Visual – Jake Beal
- 10:00-11:00 SBOL Data Model – Chris Myers
- 11:00-11:30 Coffee
- 11:30-12:00 SBOL Tools and Resources
  - SBOLStack / SBOL Shorthand / VisBOL – James McLaughlin
  - SBOLDesigner / iBioSim – Michael Zhang
  - SBOL Validator / ICE – Zach Zundel
- 12:00-01:00 Libraries
  - Java library – Chris Myers
  - JavaScript library – James McLaughlin
  - C++ & Python libraries – Bryan Bartley
- 13:00-14:00 Lunch
- 14:00-15:30 SBOL Tutorial (CRISPR/CAS9 example) – Meher Samineni
- 15:30-16:00 Coffee
- 16:00-17:30 User problems – Anil Wipat (moderator)
- 19:00 Dinner
SBOL – promoting data sharing and exchange in Synthetic Biology

Anil Wipat (on behalf of the SBOL community)
ICOS, Computing Science, Centre for Synthetic Biology and BioEconomy, Newcastle University
UK
(ico2s.org)
Standards

THREAD FORMS.

A. WHITWORTH

B. SELLERS or U.S.S.

C. B.A. British Ass'd

D. S.I. System International

E. C.E.I. Cycle Engs Institute

F. VEE American Sharp Vee

G. BRIGGS PIPE

H. LÖVENHERZ

<table>
<thead>
<tr>
<th>Type</th>
<th>Port Image</th>
<th>Connector Image</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type A</td>
<td>4.5mm x 12.0mm</td>
<td><img src="usb.png" alt="USB" /></td>
</tr>
<tr>
<td>Type B</td>
<td>7.3mm x 8.5mm</td>
<td><img src="usb.png" alt="USB" /></td>
</tr>
<tr>
<td>Mini-A</td>
<td>3.0mm x 6.8mm</td>
<td><img src="usb.png" alt="USB" /></td>
</tr>
<tr>
<td>Mini-B</td>
<td>3.0mm x 6.8mm</td>
<td><img src="usb.png" alt="USB" /></td>
</tr>
</tbody>
</table>
The nice thing about standards is that there are so many of them to choose from.

(Andrew S. Tanenbaum)
Standards

How standards proliferate:
(See A/C chargers, character encodings, instant messaging, etc)

Situation: There are 14 competing standards.

14?! Ridiculous! We need to develop one universal standard that covers everyone's use cases. Yeah!

Soon:

Situation: There are 15 competing standards.
What is SBOL – why is it needed?

* Synthetic Biology is engineering biology
* Requires movement of data & information
  * Between people, software & machines
  * Across geographic and political boundaries
* Standards needed to ensure interoperability
* SBOL - a standard way to represent information about synthetic biology designs
In 2008, a small group of researchers proposed the development of the synthetic biology open language (SBOL), an open-source standard for the exchange of genetic designs.

In 2011, the first version of the SBOL core data model was released.

In 2013, the first version of the SBOL Visual standard was released.

25+ software tools now support SBOL. Leveraging libSBOLj, etc.

ACS Synthetic Biology recommend SBOL for publications.

SBOL 2 released

libSBOLjs, libSBOLC, etc.
Essential information for synthetic DNA sequences

To the Editor:
Following a discussion by the workgroup for Data Standards in Synthetic Biology, which met in June 2010 during the Second Workshop on Biodesign Automation in Anaheim, California, we wish to highlight a problem relating to the reproducibility of the synthetic biology literature. In particular, we have noted the very small number of articles reporting synthetic gene networks that disclose the complete sequence of all the constructs they describe.

To our knowledge, there are only a few examples where full sequences have been released. In 2005, a patent application disclosed the sequences of the toggle switches published four years earlier in a paper by Gardner et al. The same year, Basu et al. deposited their construct sequences for programmed pattern formation into GenBank. Examples of synthetic DNA sequences derived from standardized parts that have been made available in GenBank include the refactored genome of the bacteriohæ"
In 2008, a small group of researchers proposed the development of the synthetic biology open language (SBOL), an open-source standard for the exchange of genetic designs.

In 2011, the first version of the SBOL core data model was released.

In 2013, the first version of the SBOL Visual standard was released.

In 2015, SBOL 2 was released.

25+ software tools now support SBOL. Leveraging libSBOLj, ACS Synthetic Biology recommend SBOL for publications.

libSBOLjs, libSBOLC, etc.
The Synthetic Biology Open Language (SBOL) provides a community standard for communicating designs in synthetic biology.

Michal Galdzicki, Kevin P Clancy, Ernst Oberortner, Matthew Pocock, Jacqueline Y Quinn, Cesar A Rodriguez, Nicholas Roehner, Mandy L Wilson, Laura Adam, J Christopher Anderson, Bryan A Bartley, Jacob Beal, Deepak Chandran, Joanna Chen, Douglas Densmore, Drew Endy, Raik Grünberg, Jennifer Hallinan, Nathan J Hillson, Jeffrey D Johnson, Allan Kuchinsky, Matthew Lux, Goksel Misirli, Jean Peccoud, Hector A Plahar + et al.

Affiliations | Contributions | Corresponding author

Received 09 November 2013 | Accepted 20 December 2013 | Published online 05 June 2014
SBOL v1

Washington

Boston University

Utah

Life Technologies

Newcastle University

Joint BioEnergy Institute

Received design file for codon optimization and gene synthesis.

Stored design and model files in repository for dissemination.

Designed four expression cassettes, leaving RBS and terminator components unspecified.

Generated four variant designs of each cassette using six RBS and six terminator components.

Assembled and modeled sixteen variant designs of the toggle switch.
In 2008, a small group of researchers proposed the development of the synthetic biology open language (SBOL), an open-source standard for the exchange of genetic designs.

In 2011, the first version of the SBOL core data model was released.

In 2013, the first version of the SBOL Visual standard was released.

25+ software tools now support SBOL Leveraging libSBOLj

ACS Synthetic Biology recommend SBOL for publications

In 2011, the first version of the SBOL core data model was released.

SBOL 2 released

libSBOLjs, libSBOLC, etc.
Synthetic Biology Open Language Visual (SBOL Visual), version 1.0.0


March 21, 2013
SBOL visual

* Open source graphical notation for SynBio designs
* SBOL 1 currently, SBOL 2 in progress
* Spec: DOI 1721.1/78349
Visual Paper

COMMUNITY PAGE

SBOL Visual: A Graphical Language for Genetic Designs

Jacqueline Y. Quinn1*, Robert Sidney Cox III2*, Aaron Adler3, Jacob Beal3, Swapnil Bhatia4, Yizhi Cai5, Joanna Chen6,7, Kevin Clancy8, Michal Galdzicki9, Nathan J. Hillson6,7, Nicolas Le Novère10, Akshay J. Maheshwari11, James Alastair McLaughlin12, Chris J. Myers13, Umesh P14, Matthew Pocock12,15, Cesar Rodriguez16, Larisa Soldatova17, Guy-Bart V. Stan18, Neil Swainston19, Anil Wipat12, Herbert M. Sauro20*.

1 Autodesk Research, Autodesk Inc., San Francisco, California, United States of America, 2 Chemical Science and Engineering, Kobe University, Kobe, Japan, 3 Information and Knowledge Technologies, Raytheon BBN Technologies, Cambridge, Massachusetts, United States of America, 4 Electrical and Computer Engineering, Boston University, Boston, Massachusetts, United States of America, 5 School of Biological Sciences, University of Edinburgh, Edinburgh, United Kingdom, 6 Fuels Synthesis and Technologies Division, Joint BioEnergy Institute, Emeryville, California, United States of America, 7 Lawrence Berkeley National Lab, Berkeley, California, United States of America, 8 Synthetic Biology Unit, ThermoFisher Scientific, Carlsbad, California, United States of America, 9 Arzeda Corp, Seattle, Washington, United States of America, 10 Babraham Institute, Cambridge, United Kingdom, 11 Stanford University School of Medicine, Stanford, California, United States of America, 12 School of Computing Science, Newcastle University, Newcastle upon Tyne, United Kingdom, 13 Department of Electrical and Computer Engineering, University of Utah, Salt Lake City, Utah, United States of America, 14 Department of Computational Biology & Bioinformatics, University of Kerala, Kerala, India, 15 Turing Ate My Hamster LTD, Newcastle upon Tyne, United Kingdom, 16 Department of Biomedical Sciences, College of Medicine, Florida State University, Tallahassee, Florida, United States of America, 17 Computer Science, Brunel University, London, United Kingdom, 18 Department of Bioengineering, Centre for Synthetic Biology and Innovation, Imperial College London, South Kensington Campus, London, United Kingdom, 19 Centre for Synthetic Biology of Fine and Specialty Chemicals (SYNBIOCHEM), University of Manchester, Manchester, United Kingdom, 20 Bioengineering, University of Washington, Seattle, Washington, United States of America.

* These authors contributed equally to this work.

hsauro@uw.edu
Example tools for the generation of SBOL Visual

* VisBOL
* PigeonCAD
* DNAplotLib

http://visbol.org/
http://pigeoncad.org/
https://github.com/VoigtLab/dnaplotlib
In 2008, a small group of researchers proposed the development of the synthetic biology open language (SBOL), an open-source standard for the exchange of genetic designs.

In 2011, the first version of the SBOL core data model was released.

In 2013, the first version of the SBOL Visual standard was released.

25+ software tools now support SBOL.

Leveraging libSBOLj, libSBOLjs, libSBOLC, etc.

ACS Synthetic Biology recommend SBOL for publications.
SBOL 2 specification
Sharing Structure and Function in Biological Design with SBOL 2.0

Nicholas Roehner, Jacob Beal, Kevin Clancy, Bryan Bartley, Goksel Misirli, Raik Grünberg, Ernst Oberortner, Matthew Pocock, Michael Bissell, Curtis Madsen, Tramy Nguyen, Michael Zhang, Zhen Zhang, Zach Zundel, Douglas Densmore, John H. Gennari, Anil Wipat, Herbert M. Sauro, and Chris J. Myers

1Department of Electrical and Computer Engineering, Boston University, Boston, Massachusetts 02215, United States
2Raytheon BBN Technologies, Cambridge, Massachusetts 02138, United States
3Thermo Fisher Scientific, Carlsbad, California 92008, United States
4Department of Bioengineering, University of Washington, Seattle, Washington 98195, United States
5School of Computing Science, Newcastle University, Newcastle upon Tyne NE1 7RU, U.K.
6Institute for Research in Immunology and Cancer, University of Montreal, Montreal, Quebec H3T 1J4, Canada
7U.S. Department of Energy Joint Genome Institute, Walnut Creek, California 94598, United States
8Turing At My Hamster, Ltd., Newcastle upon Tyne NE27 0RT, U.K.
9Amyris, Inc., Emeryville, California 94608, United States
10Department of Electrical and Computer Engineering, University of Utah, Salt Lake City, Utah 84112, United States
11Department of Bioengineering, University of Utah, Salt Lake City, Utah 84112, United States
12Department of Biomedical Informatics and Medical Education, University of Washington, Seattle, Washington 98195, United States

Supporting Information

ABSTRACT: The Synthetic Biology Open Language (SBOL) is a standard that enables collaborative engineering of biological systems across different institutions and tools. SBOL is developed through careful consideration of recent synthetic biology trends, real use cases, and consensus among leading researchers in the field and members of commercial biotechnology enterprises. We demonstrate and discuss how a set of SBOL-enabled software tools can form an integrated, cross-organizational workflow to recapitulate the design of one of the largest published genetic circuits to date, a 4-input AND sensor. This design encompasses the structural components of the system, such as its DNA, RNA, small molecules, and proteins, as well as the interactions between these components that determine the system’s behavior/function. The demonstrated workflow and resulting circuit design illustrate...
SBOL 2.0

- Sequence Annotation
- Component
- Sequence
- Context
- Module
- Participant
- Interaction
- Model

Kappa
In 2008, a small group of researchers proposed the development of the synthetic biology open language (SBOL), an open-source standard for the exchange of genetic designs.

In 2011, the first version of the SBOL core data model was released.

In 2013, the first version of the SBOL Visual standard was released.

25+ software tools now support SBOL Leveraging libSBOLj

ACS Synthetic Biology recommend SBOL for publications.

In 2011, the first version of the SBOL core data model was released.

SBOL 2 released

libSBOLjs, libSBOLC, etc.
SBOL Community

SBOL Developers Group includes 116 members from more than 30 organizations.
SBOL Community

- **SBOL Chair** – Anil Wipat (Newcastle) formerly Herbert Sauro (U. of Washington)
- **SBOL Steering Committee** – Jake Beal, Kevin Clancy, Doug Densmore, John Genari, Nathan Hilson, Chris Myers, Herbert Sauro
- **SBOL Editors** – Tramy Nguyen (Utah), Jacob Beal (BBN Technologies), Robert Sidney Cox (Kobe), Raik Grunberg (Montreal) and James McLaughlin (Newcastle).
- **Past SBOL Editors** - Michal Galdzicki (U. of Washington), Ernst Oberortner (JGI/BU), Matthew Pocock (Newcastle), Jacqueline Quinn (Google), Cesar Rodriguez (Autodesk), Nick Roehner (BU) and Mandy Wilson (VBI), Bryan Bartley (U. of Washington), Goksel Misirli (Newcastle).
In 2008, a small group of researchers proposed the development of the synthetic biology open language (SBOL), an open-source standard for the exchange of genetic designs.

In 2011, the first version of the SBOL core data model was released.

In 2013, the first version of the SBOL Visual standard was released.

25+ software tools now support SBOL.

Leveraging libSBOLj, libSBOLjs, libSBOLC, etc.

ACS Synthetic Biology recommend SBOL for publications.
Infrastructure & tools

Libraries (libSBOL)

Software libraries which import and export SBOL files are freely available at the Synthetic Biology Data Exchange on GitHub under the Apache 2.0 license. Libraries are implemented in:

- Java
- Javascript
- C/C++
- Python

All libraries are under active development. The latest release of the Java, and Javascript libraries now support SBOL 2.0. In addition a beta release of the C/C++ libraries supporting SBOL 2.0 are now available. Python bindings for SBOL 1.1 and SBOL 2.0 are currently available.
SBOL and SBML

* SBOL to SBML and back
* Misirli et al., (2011)
* Roehner et al., ACS Synthetic Biology (2013)
* Roehner et al., ACS Synthetic Biology (2014)
* Nguyen/Myers, IWBDA (2015)
## Infrastructure - applications

<table>
<thead>
<tr>
<th>Software</th>
<th>Type</th>
<th>Visual</th>
<th>Data Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>ICE</td>
<td>Repository</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>SBOL Hub</td>
<td>Repository</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>GenBank Converter</td>
<td>Helper</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>MoSeC</td>
<td>Helper</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>DNAnoveltib</td>
<td>Visualization</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Pigeon</td>
<td>Visualization</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>VisBOL</td>
<td>Visualization</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Benchling</td>
<td>DNA Design</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>DeviceEditor</td>
<td>DNA Design</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Eugene</td>
<td>DNA Design</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>GeneGenie</td>
<td>DNA Design</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>GenoCAD</td>
<td>DNA Design</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>SynBad</td>
<td>DNA Design</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>TeselaGen</td>
<td>DNA Design</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>VectorEditor</td>
<td>DNA Design</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Cello</td>
<td>Circuit Design</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>iBioSim</td>
<td>Circuit Design</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>RetroPath</td>
<td>Circuit Design</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>SBROME</td>
<td>Circuit Design</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>TinkerCell</td>
<td>Circuit Design</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>BioCompiler</td>
<td>Circuit Design</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Clotho 3.0</td>
<td>Assembly</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Raven</td>
<td>Assembly</td>
<td>Yes</td>
<td>No</td>
</tr>
</tbody>
</table>
In 2008, a small group of researchers proposed the development of the synthetic biology open language (SBOL), an open-source standard for the exchange of genetic designs.

In 2011, the first version of the SBOL core data model was released.

In 2013, the first version of the SBOL Visual standard was released.

25+ software tools now support SBOL. Leveraging libSBOLj, etc.

ACS Synthetic Biology recommend SBOL for publications.

In 2011, the first version of the SBOL core data model was released.

SBOL 2 released

libSBOLjs, libSBOLC, etc.
Publishing
ACS Synthetic Biology recommends SBOL

Improving Synthetic Biology Communication: Recommended Practices for Visual Depiction and Digital Submission of Genetic Designs

Nathan J. Hillson, Hector A. Plahar, Jacob Beal, and Ranjini Prithviraj

Fuel Synthesis and Technology Divisions, DOE Joint BioEnergy Institute (JBEI), Emeryville, California 94608, United States
Biological Systems and Engineering Division, Lawrence Berkeley National Lab, Berkeley, California 94720, United States
DOE Joint Genome Institute, Walnut Creek, California 94598, United States
Synthetic Biology Engineering Research Center, Emeryville, California 94608, United States
Raytheon BBN Technologies, Cambridge, Massachusetts 02138, United States
ACS Synthetic Biology, American Chemical Society, Washington, D.C. 20036, United States

ABSTRACT: Research is communicated more effectively and reproducibly when articles depict genetic designs consistently and fully disclose the complete sequences of all reported constructs. ACS Synthetic Biology is now providing authors with updated guidance and piloting a new tool and publication workflow that facilitate compliance with these recommended practices and standards for visual representation and data exchange.
SBOL is not just about design

- An SBOL design specified
- SBOL data should be able to travel around the SB cycle
- Capturing data as it goes
SBOL is not just about design

- AND
- Work with other standards
* SBOL is part of something bigger

* **COMBINE** an initiative to coordinate systems biology standards
  * Enables interaction with communities developing other standards
    * SBOL Visual/SBGN
    * SBOL/SBML/SED-ML
    * SBOL/BioPAX
  * Provides
    * Specification infrastructure
    * Metadata and annotations
    * COMBINE archive
    * Repositories
    * Compliance testing
COMBINE 2016

**Dates:** September 19-24, 2016  
**Location:** Newcastle upon Tyne, UK  
**Hosted by:** Newcastle University

The "Computational Modeling in Biology" Network (COMBINE) is an initiative to coordinate the development of the various community standards and formats in systems biology and related fields.

COMBINE is a workshop-style event with oral presentation, posters, and breakout sessions. The five meeting days will include talks about the COMBINE standards and associated or related standardization efforts, as well as presentations of tools using these standards. Oral presentations will be selected from the submitted abstracts. In addition to oral presentations, poster sessions will allow people to inform each other about their software and other projects in a setting that fosters interaction and in-depth discussion.

The 2016 COMBINE meeting will be held in Newcastle upon Tyne, UK from September 19 to 24, 2016: the main Workshop will run 19-23 September and an SBGN Workshop will be held on September 24.
Acknowledgements

Supported by National Science Foundation Grants CCF-1218095, DBI-1356041, and DBI-1355909
and EPSRC EP/J02175X/1

Thank you to the ICOS group, Newcastle Centre for Synthetic Biology and the BioEconomy (CSBB), and Centre for Health and Bioinformatics (CHaBi) for sponsoring dinner